

GenCore version 5.1.6
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Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using Bw model
Run on: September 17, 2003, 15:23:50 ; Search time 3936.32 Seconds

(without alignments)
16618.183 Million cell updates/sec

Title: US-10-026-106E-7
Perfect score: 1599
Sequence: 1 aaggccatgccccccca.....acatccaccqaatctatg 1599

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 288711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : GenBmbl:*

1: gb_ba:*

2: gb_ng:*

3: gb_in:*

4: gb_sm:*

5: gb_ov:*

6: gb_dat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mui:*

20: em_om:*

21: em_or:*

22: em_ovr:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_vl:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rid:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htg_hum:*

40: em_htg_mus:*

41: em_htg_other:*

RESULTS

ALIGMENTS

Result No.	Score	Query Match	Length	DB ID	Description
1	1586.4	99.2	1607	9 HSA534330	AJ534330 Homo sapi
2	1580.4	98.8	1607	9 AF493255	AF493255 Homo sapi
3	1549.4	96.9	1563	6 AX478514	AX478514 Sequence
4	1549.4	96.9	1563	9 AY129151	AY129151 Homo sapi
5	1365.4	85.4	1476	9 AY129152	AY129152 Homo sapi
6	1354.2	84.7	1476	6 AX478497	AX478497 Sequence
7	1316	82.3	1476	9 HSA534331	AJ534331 Homo sapi
8	1086.8	68.0	1560	6 AX478524	AX478524 Sequence
9	916.2	57.3	1473	6 AX478499	AX478499 Sequence
10	794.4	49.7	1608	10 AX184376	AL59083 Human DNA
11	783.8	49.0	1608	6 AX478528	AY184376 Mus muscu
12	609.4	38.1	1922	6 AX478518	AX478528 Sequence
13	607.4	38.1	1922	10 AX184376	AX478518 Sequence
14	498	31.1	674	6 AX478516	AX478516 Sequence
15	498	31.1	674	9 AY19153	AY19153 Homo sapi
16	498	31.1	704	6 AX478525	AX478525 Sequence
17	351.2	22.0	633	6 AX478525	AX478525 Sequence
18	335.4	21.0	374	6 AX059744	AL662311 Mouse DNA
19	326.6	20.4	165515	10 AL662311	AL662311 Mouse DNA
20	297	18.6	214062	2 AC123354	AC123354 Rattus no
21	297	18.6	268510	2 AC123354	AC123354 Rattus no
22	165	10.3	392	6 AX070906	AK070906 Sequence
23	163.4	10.2	382	6 AX070806	AK070806 Sequence
24	24	4.3	321	6 RNQ230590	AY070890 Rattus no
25	25	4.1	125020	9 AF429315	AF429315 Homo sapi
26	25	3.6	125020	9 AF429315	AF429315 Homo sapi
27	27	49.4	3.1	124856	2 AC119792 Rattus no
28	28	49.2	3.1	213335	2 AC141961 Rattus no
29	29	48.8	3.1	242385	2 AC103353 Rattus no
30	30	47.4	3.0	2000	6 AX655393 Sequence
31	31	47.4	3.0	220498	2 AC111813 Rattus no
32	32	47.2	3.0	110000	2 AC144914_1 Continuation (2 of
33	33	47.2	3.0	176789	2 AC032013 Mbo mbcu
34	34	47.2	3.0	217092	10 AL590988 Human DNA
35	35	47	2.9	227202	2 AC128501 Rattus no
36	36	46.8	2.9	227182	2 AC099283 Rattus no
37	37	46.6	2.9	243648	2 AC128576 Rattus no
38	38	46.2	2.9	216511	2 AC123662 Mus muscu
39	39	46	2.9	242857	2 AC096180 Rattus no
40	40	45.8	2.9	260809	2 AC126820 Rattus no
41	41	45.8	2.9	286135	2 AC112570 Rattus no
42	42	45.2	2.8	22998	2 AC109723 Rattus no
43	43	45	2.8	229414	2 AC126951 Rattus no
44	44	44.8	2.8	210470	2 AC127779 Rattus no
45	45	44.4	2.8	3120	9 AF133086 Homo sapi

REFERENCE
AUTHORS
TITLE

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Cloning of a new type II cytokine receptor activating signal.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30), an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Eml; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WormPep database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep. This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/Projects/Chromosome1/>. RPL1-10N16 is from the library RPLC1-11 constructed by the group of Piefer de Jong. For further details see <http://www.chori.org/bacpac/home.htm>. VECTOR; pBACe3.6

This sequence is the entire insert of clone RPL1-10N16. The true left end of clone RPL1-509F14 is at 11440 in this sequence. The true right end of clone RPL1-293P20 is at 7865 in this sequence. location/Qualifiers 1..164684

source /organism="Homo sapiens"

mol_type="genomic DNA"

/db_xref="taxon:9606"

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/clone_lbm="RPLC1-11.1"

51656..51817

/notes="Sequence from overlapping clone RPL1-509F14 (AL358412). Assembly confirmed by restriction digest." 76735..77049

/notes="Single clone region. Read generated from a transposon library derived from a single PUC clone. Restriction digest data confirm the assembly." 1294

1446 GAGGAGAGAGGAGGAGGAATCAGAAATTGAGCACGGATGCCAGTGCGGG 1505

Db 1354 GARGARGARGARGCNCNMGNGNMGARGWSNARGATGAROWAYNGAVGCGN 1413

Qy 1505 GCTGAGGACCCGAGGAGGAGGAGCAGGGCGGAGATGGGCCATACGCCAG 1564

Db 1414 GCGNARSNACNCAKGNAENGARGAYWNGNGNANCYNGCAYVAYGCGN 1472

RESULT 10

AL590683/c

LOCUS AL590683 164684 bp DNA linear PRI 01-FEB-2002

DEFINITION Human DNA sequence from clone RP11-10N16 on chromosome 1, complete

ACCESSION AL590683

VERSION AL590683.16 GI:18476679

KEYWORDS RTG.

ORGANISM Homo sapiens (human)

Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 164684)

AUTHORS Chapman,J.

JOURNAL Direct Submission

Submitted (01-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clonesnew@sanger.ac.uk

COMMENT On Feb 1, 2002 this sequence version replaced 91:18135066.

FEATURES

source

BASE COUNT

ORIGIN

Query Match, Best Local Similarity 49.7%, Score 794.4, DB 9, Length 164684; Matches 795; Conservative 0, Mismatches 1, Indels 0, Gaps 0;

Qy 804 CTGACTTTCGGACACACACCTTGTGCAACCTTGTGCCAGGACAGATC 863

Db 22493 CAGCACTTTCGGACACACACCTTGTGCAACCTTGTGCCAGGACAGATC 22434

Qy 864 GGAATGACTTCCTCTGTCACACCCCTTGCAACCTTGTGCCAGGACAGATC 923

Db 22433 GGAATGACTTCCTCTGTCACACCCCTTGCAACCTTGTGCCAGGACAGATC 22434

Qy 924 CGATCGGGGCCGCCACCCACACAGACAGATGAGAGAGGAGCTTGAGAGAGA 983

Db 22373 CGATCGGGGCCGCCACCCACACAGACAGATGAGAGAGGAGCTTGAGAGAGA 22314

Qy 984 GAGGAGAGGATGAGGAGACAGAGAGATGCGTCAGTTCAGCTTCAAGGCTTACATGACCA 1043

Db 22213 GAGGAGAGGATGAGGAGACAGAGAGATGCGTCAGTTCAGCTTCAAGGCTTACATGACCA 22254

Qy 1044 CCTTCTTCGGGCCAGAGACACCGCTCGCAAGGACTCTGGAGGTGGGGGAGC 1103

Db 22253 CCTTCTTCGGGCCAGAGACACCGCTCGCAAGGACTCTGGAGGTGGGGGAGC 22194

Db	1865	AGCCCCACCTCTCTGCTGGAGCTCCAGAACGCACTGGGTT	1912	Qy	486	GCATTCTGGAGGGGGCCGAGAACAGACCCATTCCACTCACTCCCATGCCCCAG	545
RESULT	13			Db	529	GCATTCGAGGGGGGGCGAGAACAGACCCATTCCACTCACTCCCATGCCCCAG	583
AX478518		AX478518	Sequence 22 from Patent WO244209.	Qy	546	CCAGTCAGAGTACTCTCAGCAGCTGCGAGACGACTGCCTCAGTCAGTCAGACCC	605
LOCUS			ACCESSION AX478518	Db	589	CCAGTCAGAGTACTCTCAGCAGCTGCGAGACGACTGCCTCAGTCAGTCAGACCC	643
DEFINITION			VERSION AX478518.1	Qy	606	ATCTACAGCTTCAGTGCCGAAATCAGAGCTGAGCTCTAAGGCCACTGTCTGCTG	665
KEYWORDS			JOURNAL Patent: WO 0244209-A 22 06-JUN-2002;	Db	649	ATCTACAGCTTCAGTGCCGAAATCAGAGCTGAGCTCTAAGGCCACTGTCTGCTG	708
SOURCE			ZymoGenetics, Inc. (US)	Qy	666	GAGGTCCAGAGGAGACTGG	686
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RESULT 15

AY129153

LOCUS AY129153

Hom sapiens- interleukin 674 bp mRNA linear PRI 26-NOV-2002

mRNA, complete cds; alternatively spliced.

ACCESSION AY129153

VERSION AY129153.1 GI:25527135

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 674)

AUTHORS Shepard,P.O., Presnell,S.R., Fox,B.A., Gilbert,T., Haldeman,B.A. and Grant,F.J.

TITLE IL2RA splice variant 3

REFERENCE 2 (bases 1 to 674)

AUTHORS Shepard,P.O., Presnell,S.R., Fox,B.A., Gilbert,T., Haldeman,B.A. and Grant,F.J.

TITLE Direct Submission

JOURNAL Submitted (05-JUL-2002) Bioinformatics, ZymoGenetics, Inc., 1201 Eastlake Avenue East, Seattle, WA 98102; USA

FEATURES

SOURCE

1. . 674

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9605"

gene

1. . 674

/gene="IL2RA"

CDS.

1. . 636

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/notes="alternatively spliced"

/codon_start=1

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/protein_id="AAH2868.1"

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BASE COUNT

ORIGIN

128 a 223 c 182 g 141 t

Query Match 31.1%; Score 498; DB 9; Length 674;

Best Local Similarity 99.8%; Pred. No. 4e-17; Matches 509; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 7 ATGGGGGAGCCGAGCGCTGGAGGCCCTGTCCTGCTGAGGCCCTCAGGG 66

Db 1 ATGGGGGAGCCGAGCGCTGGAGGCCCTGTCCTGCTGAGGCCCTCAGGG 60

QY 486 GCATTCGAGGAGGGGGCGGAAACAG 515

Db 481 GCATTCGAGGAGGGGGCGGAAACAG 510